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TECH CENTER 1600280



1600

RAW SEQUENCE LISTING

DATE: 04/03/2003

PATENT APPLICATION: US/09/866,379B

TIME: 14:43:53

Input Set : A:\09010-029006.txt

Output Set: N:\CRF4\04032003\I866379B.raw

4 <110> APPLICANT: Short, Jay M.
5 Kretz, Keith A.
6 Gray, Kevin A.
7 Barton, Nelson Robert
8 Garrett, James E.
9 O'Donoghue, Eileen
10 Mathur, Eric C.
11 <110> TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES
12 THEREOF
13 <120> FILE REFERENCE: 09010-029006
14 <130> CURRENT APPLICATION NUMBER: US 09/866,379B
15 <141> CURRENT FILING DATE: 2001-06-24
16 <150> PRIOR APPLICATION NUMBER: US 09/580,515
17 <161> PRIOR FILING DATE: 2000-05-25
18 <170> PRIOR APPLICATION NUMBER: US 09/318,528
19 <181> PRIOR FILING DATE: 1999-05-15
20 <190> PRIOR APPLICATION NUMBER: US 09/291,931
21 <201> PRIOR FILING DATE: 1999-04-13
22 <210> PRIOR APPLICATION NUMBER: US 09/259,214
23 <221> PRIOR FILING DATE: 1999-03-01
24 <230> PRIOR APPLICATION NUMBER: US 08/910,798
25 <241> PRIOR FILING DATE: 1997-06-13
26 <260> NUMBER OF SEQ ID NOS: 10
27 <270> SOFTWARE: FastSeq for Windows Version 4.0
28 <280> SEQ ID NO: 1
29 <291> LENGTH: 1320
30 <300> TYPE: DNA
31 <310> ORGANISM: Escherichia coli
32 <320> FEATURE:
33 <331> NAME/KEY: CDS
34 <332> LOCATION: (1)...(1320)
35 <333> NAME/KEY: misc feature
36 <334> LOCATION: 116
37 <335> OTHER INFORMATION: n = A,T,C or G

W--> 52 <400> 1

53	atg aag aag atg atg tta atg cca ttt tta ttt ctt ctg att ccg tta acc	48
54	Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr	
55	1 10 15	
56	ccg caa ttt gaa ttt ggt cag agt gag ccg gag ctg aag ctg gaa agt	96
57	Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser	
58	20 25 30	
59	gtg gtc att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg	144
60	Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr	

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63          35          40          45
65 caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg cgg gta 192
66 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
67          50          55          60
W--> 69 aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc tat ctc 240
70 Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Gln Leu Ile Ala Tyr Leu
71 65          70          75          80
73 gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg gcg aaa 288
74 Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
75          85          90          95
77 aag ggc tgc cgg cag tct ggt cag gtc gcc att att gct gat gtc gac 336
78 Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
79          100          105          110
81 gag cgt acc cgt aaa aca gcc gaa gcc ttc gcc gcc ggg ctg gca cct 384
82 Glu Arg Thr Arg Lys Thr Gly Gln Ala Pro Ala Ala Gly Leu Ala Pro
83          115          120          125
85 gac tgt gca ata acc gta cat acc cag gca gat acc tcc agt ccc gat 432
86 Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
87          130          135          140
89 cgg tta ttt aat cct cta aaa aat ggc gtt tgc caa ctg gat aac ggg 480
90 Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
91 145          150          155          160
93 aac gtg act gac ggg atc ctc agc agg gca gga ggg tca att gct gac 528
94 Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp
95          165          170          175
97 ttt acc ggg cat cgg caa aag ggt ttt cgg gaa ctg gaa cgg gtg ctt 576
98 Pro Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
99          180          185          190
101 aat ttt cgg caa tca aac ttg tgc ctt aaa cgt gag aca cag gac caa 624
102 Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
103          195          200          205
105 agc tgt tca tta aag cag gca tta cca tgg gaa ctc aag gtg agc gcc 672
106 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
107          210          215          220
109 gac aat gtc tca tta acc ggt ggg gta agc ctc gca tca atg ctg aag 720
110 Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
111 225          230          235          240
113 gag ata ttt ctc ctg caa caa gca cag gga atg cgg gag cgg ggg tgg 768
114 Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
115          245          250          255
117 gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat 816
118 Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
119          260          265          270
121 aac ggg caa ttt tat ttg cta caa cgg aag cca gag gtt gcc cgc agc 864
122 Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
123          275          280          285
125 cgc gcc acc cgg tta ttg gat ttg atc atg gca ggg ttg aag ccc cat 912
126 Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His
127          290          295          300

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```

129 cca ccg caa saa cag cgc tat ggt gtg aca tta ccc act tca gta ctg      960
130 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
131 305      310      315      320
132 att acc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg      1008
133 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
134 325      330      335
135 cag ctg aac tgg agc att ccc ggt cag ccc gat aac acc ccc cca ggt      1056
136 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
137 340      345      350
138 ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag      1104
139 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
140 355      360      365
141 agc att cag gtt tgg ctg gtc ttc cag act tta cag cag atg cgt gat      1152
142 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
143 370      375      380
144 aac acc ccc ctg tca tta aat acc ccc ccc gga gag gtc aac ctg acc      1200
145 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
146 385      390      395      400
147 ctg gca gga tgt gaa gag cga aat ccc cag ggc atg tgt tgg ttg gaa      1248
148 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
149 405      410      415
150 att att acc caa atc gtg aat gaa gca cgc ata ccc ggc tgc agt ctg      1296
151 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
152 420      425      430
153 aga tct cat cac cat cac cat cac caa      1323
154 Arg Ser His His His His His His
155 435      440
156 110 SEQ ID NO: 2
157 441 LENGTH: 440
158 442 TYPE: PRT
159 443 ORGANISM: Escherichia coli
160 444 SEQUENCE: 2
161 Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
162 1 5 10 15
163 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
164 20 25 30
165 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
166 35 40 45
167 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
168 50 55 60
169 Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
170 65 70 75 80
171 Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
172 85 90 95
173 Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
174 100 105 110
175 Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
176 115 120 125
177 Arg Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp

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```

189      130      135      140
190 Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
191 145      150      155      160
192 Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp
193      165      170      175
194 Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
195      180      185      190
196 Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
197      195      200      205
198 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
199      210      215      220
200 Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
201 225      230      235      240
202 Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
203      245      250      255
204 Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
205      260      265      270
206 Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
207      275      280      285
208 Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His
209      290      295      300
210 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
211 305      310      315      320
212 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
213      325      330      335
214 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
215      340      345      350
216 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
217      355      360      365
218 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
219      370      375      380
220 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
221 385      390      395      400
222 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
223      405      410      415
224 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
225      420      425      430
226 Arg Ser His His His His His His
227      435      440
229 <210> SEQ ID NO: 3
230 <211> LENGTH: 49
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: primer
237 <400> SEQUENCE: 3
238 gtttttgaaat tcaaggagga atttaaataa aagagatatt aatccatt
240 <210> SEQ ID NO: 4
241 <211> LENGTH: 33

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RAW SEQUENCE LISTING

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Input Set : A:\09010-029006.txt

Output Set: N:\CRF4\04032003\I866379B.raw

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242 <210> TYPE: DNA
243 <211> ORGANISM: Artificial Sequence
244 <212> FEATURE:
245 <213> OTHER INFORMATION: primer
246 <214> SEQUENCE: 4
249 gttttctggat ccttacaac tgcacgocgg tat          23
251 <215> SEQ ID NO: 5
252 <216> LENGTH: 1901
253 <217> TYPE: DNA
254 <218> ORGANISM: Escherichia coli
255 <219> FEATURE:
256 <220> NAME/KEY: misc_feature
257 <221> LOCATION: 403
258 <222> OTHER INFORMATION: n = A,T,C or G
261 <223> SEQUENCE: 5
262 taaggagcag aaacaatgtg gtatttaact tggttogtgg gcattttggt gatgtgttgg          60
263 ctctccaccc ttgtgttggg atgggtggac ccggtgttga aaagttaaag aaagttaggc          120
264 ttatctgggg cattagcctc gcctcaggca atcaataatg tcagatatga aaagcggaaa          180
265 ctatctgatg aaagcctctt taatccattt ttatctcttt ctgatttcgt taaacccgca          240
266 atctgcttcc cctcagagtg agccggagct gaagctggaa agtgtgttga ttgtcagtg          300
267 tttgtgtgtg cgtgctccaa ccaaggccac gcaactgatg caggatgtca ccccaagcgc          360
W--> 268 atggccaacc tggccggtaa aactgggtga gctgacaccg cnggtgtgtg agctaatacg          420
269 ctattcttga cattacaac gccagcgtct ggtagccgac ggatttgttg cgaaaaaagg          480
270 ctctccaccc ttgtgttggg atgggtggac ccggtgttga aaagttaaag aaagttaggc          540
271 ttatctgggg cattagcctc gcctcaggca atcaataatg tcagatatga aaagcggaaa          600
272 ctatctgatg aaagcctctt taatccattt ttatctcttt ctgatttcgt taaacccgca          660
273 atctgcttcc cctcagagtg agccggagct gaagctggaa agtgtgttga ttgtcagtg          720
274 ttatctgggg cattagcctc gcctcaggca atcaataatg tcagatatga aaagcggaaa          780
275 ctatctgatg aaagcctctt taatccattt ttatctcttt ctgatttcgt taaacccgca          840
276 atctgcttcc cctcagagtg agccggagct gaagctggaa agtgtgttga ttgtcagtg          900
277 ttatctgggg cattagcctc gcctcaggca atcaataatg tcagatatga aaagcggaaa          960
278 ctatctgatg aaagcctctt taatccattt ttatctcttt ctgatttcgt taaacccgca          1020
279 atctgcttcc cctcagagtg agccggagct gaagctggaa agtgtgttga ttgtcagtg          1080
280 ttatctgggg cattagcctc gcctcaggca atcaataatg tcagatatga aaagcggaaa          1140
281 ctatctgatg aaagcctctt taatccattt ttatctcttt ctgatttcgt taaacccgca          1200
282 atctgcttcc cctcagagtg agccggagct gaagctggaa agtgtgttga ttgtcagtg          1260
283 ttatctgggg cattagcctc gcctcaggca atcaataatg tcagatatga aaagcggaaa          1320
284 ctatctgatg aaagcctctt taatccattt ttatctcttt ctgatttcgt taaacccgca          1380
285 atctgcttcc cctcagagtg agccggagct gaagctggaa agtgtgttga ttgtcagtg          1440
286 ttatctgggg cattagcctc gcctcaggca atcaataatg tcagatatga aaagcggaaa          1500
287 ctatctgatg aaagcctctt taatccattt ttatctcttt ctgatttcgt taaacccgca          1560
288 atctgcttcc cctcagagtg agccggagct gaagctggaa agtgtgttga ttgtcagtg          1620
289 ttatctgggg cattagcctc gcctcaggca atcaataatg tcagatatga aaagcggaaa          1680
290 ctatctgatg aaagcctctt taatccattt ttatctcttt ctgatttcgt taaacccgca          1740
291 atctgcttcc cctcagagtg agccggagct gaagctggaa agtgtgttga ttgtcagtg          1800
292 ttatctgggg cattagcctc gcctcaggca atcaataatg tcagatatga aaagcggaaa          1860
293 ctatctgatg aaagcctctt taatccattt ttatctcttt ctgatttcgt taaacccgca          1901
294 <215> SEQ ID NO: 6
295 <216> LENGTH: 1901

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/866,379B

DATE: 04/03/2003
TIME: 14:43:54

Input Set : A:\09010-029006.txt
Output Set: N:\CRF4\04032003\I866379B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 216
Seq#:5; N Pos. 403
Seq#:6; N Pos. 403
Seq#:7; N Pos. 403

VERIFICATION SUMMARY

DATE: 04/03/2003

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TIME: 14:43:54

Input Set : A:\09010-029006.txt

Output Set: N:\CRF4\04032003\I866379B.raw

L:52 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:192
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:360
L:312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:360
L:352 M:358 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:373
L:545 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:548 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9